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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/799,910

DATE: 11/26/97  
TIME: 13:57:20

INPUT SET: S21738.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

ENTERED

1  
2  
3 (1) General Information  
4  
5 (i) APPLICANT: Falb, Dean  
6  
7 (ii) TITLE OF THE INVENTION: COMPOSITIONS AND METHODS FOR  
8 THE TREATMENT AND DIAGNOSIS OF  
9 CARDIOVASCULAR DISEASE  
10  
11 (iii) NUMBER OF SEQUENCES: 44  
12  
13 (iv) CORRESPONDENCE ADDRESS:  
14 (A) ADDRESSEE: PENNIE & EDMONDS LLP  
15 (B) STREET: 1155 Avenue of the Americas  
16 (C) CITY: New York  
17 (D) STATE: NY  
18 (E) COUNTRY: USA  
19 (F) ZIP: 10036-2711  
20  
21 (v) COMPUTER READABLE FORM:  
22 (A) MEDIUM TYPE: Diskette  
23 (B) COMPUTER: IBM Compatible  
24 (C) OPERATING SYSTEM: DOS  
25 (D) SOFTWARE: FastSEQ Version 2.0  
26  
27 (vi) CURRENT APPLICATION DATA:  
28 (A) APPLICATION NUMBER: 08/799,910  
29 (B) FILING DATE: 13-FEB-1997  
30 (C) CLASSIFICATION:  
31  
32 (vii) PRIOR APPLICATION DATA:  
33 (A) APPLICATION NUMBER: 60/011,787  
34 (B) FILING DATE: 16-FEB-1996  
35  
36  
37  
38 (viii) ATTORNEY/AGENT INFORMATION:  
39 (A) NAME: Coruzzi, Laura A  
40 (B) REGISTRATION NUMBER: 30,742  
41 (C) REFERENCE/DOCKET NUMBER: 7853-067-999  
42  
43 (ix) TELECOMMUNICATION INFORMATION:  
44 (A) TELEPHONE: (212)7909090  
45 (B) TELEFAX: (212)8699741  
46 (C) TELEX: 66141 PENNIE

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/799,910

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47

48

49

(2) INFORMATION FOR SEQ ID NO:1:

50

51

(i) SEQUENCE CHARACTERISTICS:

52

(A) LENGTH: 1953 base pairs

53

(B) TYPE: nucleic acid

54

(C) STRANDEDNESS: both

55

(D) TOPOLOGY: linear

56

57

(ii) MOLECULE TYPE: cDNA

58

(ix) FEATURE:

59

60

(A) NAME/KEY: Coding Sequence

61

(B) LOCATION: 162...1871

62

(D) OTHER INFORMATION:

63

64

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

66

67

GGCACGAGTC GGAGCCGGGC GGAGGGGAGG GGGGAAAGAG GAGCGCAGGG TGAGAGTGAG 60

68

CCGCAGGCTT CGGGAGGCGA GGGGGCGGGG GGAGCAGCGC CGAGGYCGCC GCCTCCGCCT 120

69

CCGCCGCTA GGACTAGGGG GTGGGGGACG GACAAGCCCC G ATG CCG GGG GAG ACG 176

70

Met Pro Gly Glu Thr

71

1

5

72

73

GAA GAG CCG AGA CCC CCG GAG CAG CAG GAC CAG GAA GGG GGA GAG GCG 224

74

Glu Glu Pro Arg Pro Pro Glu Gln Gln Asp Gln Glu Gly Gly Glu Ala

75

10

15

20

76

77

GCC AAG GCG GCT CCG GAG GAG CCC CAA CAA CGG CCC CCT GAG GCG GTC 272

78

Ala Lys Ala Ala Pro Glu Glu Pro Gln Gln Arg Pro Pro Glu Ala Val

79

25

30

35

80

81

GCG GCG GCG CCT GCA GGG ACC ACT AGC AGC CGC GTG CTG AGG GGA GGT 320

82

Ala Ala Ala Pro Ala Gly Thr Thr Ser Ser Arg Val Leu Arg Gly Gly

83

40

45

50

84

85

CGG GAC CGA GGC CGG GCC GCT GCG GCC GCC GCC GCC GCA GCT GTG TCC 368

86

Arg Asp Arg Gly Arg Ala Ala Ala Ala Ala Ala Ala Ala Val Ser

87

55

60

65

88

89

CGC CGG AGG AAG GCC GAG TAT CCC CGC CGG CGG AGG AGC AGC CCC AGC 416

90

Arg Arg Arg Lys Ala Glu Tyr Pro Arg Arg Arg Arg Ser Ser Pro Ser

91

70

75

80

85

92

93

GCC AGG CCT CCC GAC GTC CCC GGG CAG CAG CCC CAG GCC GCG AAG TCC 464

94

Ala Arg Pro Pro Asp Val Pro Gly Gln Gln Pro Gln Ala Ala Lys Ser

95

90

95

100

96

97

CCG TCT CCA GTT CAG GGC AAG AAG AGT CCG CGA CTC CTA TGC ATA GAA 512

98

Pro Ser Pro Val Gln Gly Lys Lys Ser Pro Arg Leu Leu Cys Ile Glu

99

105

110

115

**INPUT SET: S21738.raw**

100																		
101	AAA	GTA	ACA	ACT	GAT	AAA	GAT	CCC	AAG	GAA	GAA	AAA	GAG	GAA	GAA	GAC		560
102	Lys	Val	Thr	Thr	Asp	Lys	Asp	Pro	Lys	Glu	Glu	Lys	Glu	Glu	Glu	Asp		
103			120					125					130					
104																		
105	GAT	TCT	GCC	CTC	CCT	CAG	GAA	GTT	TCC	ATT	GCT	GCA	TCT	AGA	CCT	AGC		608
106	Asp	Ser	Ala	Leu	Pro	Gln	Glu	Val	Ser	Ile	Ala	Ala	Ser	Arg	Pro	Ser		
107		135					140					145						
108																		
109	CGG	GGC	TGG	CGT	AGT	AGT	AGG	ACA	TCT	GTT	TCT	CGC	CAT	CGT	GAT	ACA		656
110	Arg	Gly	Trp	Arg	Ser	Ser	Arg	Thr	Ser	Val	Ser	Arg	His	Arg	Asp	Thr		
111	150					155					160					165		
112																		
113	GAG	AAC	ACC	CGA	AGC	TCT	CGG	TCC	AAG	ACC	GGT	TCA	TTG	CAG	CTC	ATT		704
114	Glu	Asn	Thr	Arg	Ser	Ser	Arg	Ser	Lys	Thr	Gly	Ser	Leu	Gln	Leu	Ile		
115					170					175					180			
116																		
117	TGC	AAG	TCA	GAA	CCA	AAT	ACA	GAC	CAA	CTT	GAT	TAT	GAT	GTT	GGA	GAA		752
118	Cys	Lys	Ser	Glu	Pro	Asn	Thr	Asp	Gln	Leu	Asp	Tyr	Asp	Val	Gly	Glu		
119				185				190						195				
120																		
121	GAG	CAT	CAG	TCT	CCA	GGT	GGC	ATT	AGT	GGT	GAA	GAG	GAA	GAG	GAG	GAG		800
122	Glu	His	Gln	Ser	Pro	Gly	Gly	Ile	Ser	Gly	Glu	Glu	Glu	Glu	Glu	Glu		
123			200					205					210					
124																		
125	GAA	GAA	GAG	ATG	TTA	ATC	AGT	GAA	GAG	GAG	ATA	CCA	TTC	AAA	GAT	GAT		848
126	Glu	Glu	Glu	Met	Leu	Ile	Ser	Glu	Glu	Glu	Ile	Pro	Phe	Lys	Asp	Asp		
127		215					220					225						
128																		
129	CCA	AGA	GAT	GAG	ACC	TAC	AAA	CCC	CAC	TTA	GAA	AGG	GAA	ACC	CCA	AAG		896
130	Pro	Arg	Asp	Glu	Thr	Tyr	Lys	Pro	His	Leu	Glu	Arg	Glu	Thr	Pro	Lys		
131	230					235					240					245		
132																		
133	CCA	CGG	AGA	AAA	TCA	GGG	AAG	GTA	AAA	GAA	GAG	AAG	GAG	AAG	AAG	GAA		944
134	Pro	Arg	Arg	Lys	Ser	Gly	Lys	Val	Lys	Glu	Glu	Lys	Glu	Lys	Lys	Glu		
135					250					255					260			
136																		
137	ATT	AAA	GTG	GAA	GTA	GAG	GTG	GAG	GTG	AAA	GAA	GAG	GAG	AAT	GAA	ATT		992
138	Ile	Lys	Val	Glu	Val	Glu	Val	Glu	Val	Lys	Glu	Glu						

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153	CGC TAT TTG CAG CAC CAC ATT AAA TAC CAG CAT TTG CTG AAG AAG AAA	1184
154	Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys Lys	
155	330 335 340	
156		
157	TAT GTA TGT CCC CAT CCC TCC TGT GGA CGA CTC TTC AGG CTT CAG AAG	1232
158	Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln Lys	
159	345 350 355	
160		
161	CAA CTT CTG CGA CAT GCC AAA CAT CAT ACA GAT CAA AGG GAT TAT ATC	1280
162	Gln Leu Leu Arg His Ala Lys His His Thr Asp Gln Arg Asp Tyr Ile	
163	360 365 370	
164		
165	TGT GAA TAT TGT GCT CGG GCC TTC AAG AGT TCC CAC AAT CTG GCA GTG	1328
166	Cys Glu Tyr Cys Ala Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val	
167	375 380 385	
168		
169	CAC CGG ATG ATT CAC ACT GGC GAG AAG CCA TTA CAA TGT GAG ATC TGT	1376
170	His Arg Met Ile His Thr Gly Glu Lys Pro Leu Gln Cys Glu Ile Cys	
171	390 395 400 405	
172		
173	GGA TTT ACT TGT CGA CAA AAG GCA TCT CTT AAT TGG CAC ATG AAG AAA	1424
174	Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu Asn Trp His Met Lys Lys	
175	410 415 420	
176		
177	CAT GAT GCA GAC TCC TTC TAC CAG TTT TCT TGC AAT ATC TGT GGC AAA	1472
178	His Asp Ala Asp Ser Phe Tyr Gln Phe Ser Cys Asn Ile Cys Gly Lys	
179	425 430 435	
180		
181	AAA TTT GAG AAG AAG GAC AGC GTA GTG GCA CAC AAG GCA AAA AGC CAC	1520
182	Lys Phe Glu Lys Lys Asp Ser Val Val Ala His Lys Ala Lys Ser His	
183	440 445 450	
184		
185	CCT GAG GTG CTG ATT GCA GAA GCT CTG GCT GCC AAT GCA GGC GCC CTC	1568
186	Pro Glu Val Leu Ile Ala Glu Ala Leu Ala Ala Asn Ala Gly Ala Leu	
187	455 460 465	
188		
189	ATC ACC AGC ACA GAT ATC TTG GGC ACT AAC CCA GAG TCC CTG ACG CAG	1616
190	Ile Thr Ser Thr Asp Ile Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln	
191	470 475 480 485	
192		
193	CCT TCA GAT GGT CAG GGT CTT CCT CTT CTT CCT GAG CCC TTG GGA AAC	1664
194	Pro Ser Asp Gly Gln Gly Leu Pro Leu Leu Pro Glu Pro Leu Gly Asn	
195	490 495 500	
196		
197	TCA ACC TCT GGA GAG TGC CTA CTG TTA GAA GCT GAA GGG ATG TCA AAG	1712
198	Ser Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser Lys	
199	505 510 515	
200		
201	TCA TAC TGC AGT GGG ACG GAA CGG GTG AGC CTG ATG GCT GAT GGG AAG	1760
202	Ser Tyr Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys	
203	520 525 530	
204		
205	ATC TTT GTG GGA AGC GGC AGC AGT GGA GGC ACT GAA GGG CTG GTT ATG	1808

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/799,910

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206 Ile Phe Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met  
207 535 540 545  
208  
209 AAC TCA GAT ATA CTC GGT GCT ACC ACA GAG GTT CTG ATT GAA GAT TCA 1856  
210 Asn Ser Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser  
211 550 555 560 565  
212  
213 GAC TCT GCC GGA CCT TAGTGGACAG GAAGACTTGG GGCATGGGAC AGCTCAGACT T 1912  
214 Asp Ser Ala Gly Pro  
215 570  
216  
217 TGTATTTAAA AGTTAAAAAG GACAAAAAAA AAAAAAAAAA A 1953  
218  
219  
220

## (2) INFORMATION FOR SEQ ID NO:2:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

### (ii) MOLECULE TYPE: protein

### (v) FRAGMENT TYPE: internal

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

231  
232 Met Pro Gly Glu Thr Glu Glu Pro Arg Pro Pro Glu Gln Gln Asp Gln  
233 1 5 10 15  
234 Glu Gly Gly Glu Ala Ala Lys Ala Ala Pro Glu Glu Pro Gln Gln Arg  
235 20 25 30  
236 Pro Pro Glu Ala Val Ala Ala Ala Pro Ala Gly Thr Thr Ser Ser Arg  
237 35 40 45  
238 Val Leu Arg Gly Gly Arg Asp Arg Gly Arg Ala Ala Ala Ala Ala  
239 50 55 60  
240 Ala Ala Ala Val Ser Arg Arg Arg Lys Ala Glu Tyr Pro Arg Arg Arg  
241 65 70 75 80  
242 Arg Ser Ser Pro Ser Ala Arg Pro Pro Asp Val Pro Gly Gln Gln Pro  
243 85 90 95  
244 Gln Ala Ala Lys Ser Pro Ser Pro Val Gln Gly Lys Lys Ser Pro Arg  
245 100 105 110  
246 Leu Leu Cys Ile Glu Lys Val Thr Asp Lys Asp Pro Lys Glu Glu  
247 115 120 125  
248 Lys Glu Glu Glu Asp Asp Ser Ala Leu Pro Gln Glu Val Ser Ile Ala  
249 130 135 140  
250 Ala Ser Arg Pro Ser Arg Gly Trp Arg Ser Ser Arg Thr Ser Val Ser  
251 145 150 155 160  
252 Arg His Arg Asp Thr Glu Asn Thr Arg Ser Ser Arg Ser Lys Thr Gly  
253 165 170 175  
254 Ser Leu Gln Leu Ile Cys Lys Ser Glu Pro Asn Thr Asp Gln Leu Asp  
255 180 185 190  
256 Tyr Asp Val Gly Glu Glu His Gln Ser Pro Gly Gly Ile Ser Gly Glu  
257 195 200 205  
258 Glu Glu Glu Glu Glu Glu Glu Met Leu Ile Ser Glu Glu Glu Ile

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/799,910**

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Line

Error

Original Text